We claim:

1. A multidomain method for evaluating parameters of a semiconductor wafer or wafer set comprising:

identifying a group of semiconductor wafer parameters to be evaluated;

mapping the semiconductor wafer parameters into at least one genotype, said genotype comprising a collection of genes, each gene corresponding to a selected one of the group of semiconductor wafer parameters to be evaluated;

defining more than one domain as a collection of genotypes, each domain with its own population of genotypes;

deriving a set of theoretical data for each genotype;

inspecting the semiconductor wafer or wafer set using a beam of radiation and generating therefrom sets of measured data;

comparing a set of measured data to a corresponding set of derived theoretical data for each genotype in each domain in order to determine a level of fitness for each genotype;

migrating genotypes among the domains by selecting at least one genotype from a current domain population and adding it to the population of a different domain;

evolving a next population for each domain by selecting at least one genotype from the current population based on the fitness level of the genotype and performing a genetic operation on the at least one genotype, thereby creating at least one new genotype and adding the at least one new genotype to the next population; and

repeating the comparing, migrating, and evolving steps so that for each domain the fittest genotype becomes increasingly more fit.

2. A method as recited in claim 1 wherein the likelihood of selecting a genotype for a genetic operation from a domain population is proportional to the degree to which the derived theoretical data

associated with that genotype matches the measured data.

3. A method as recited in claim 1 wherein the likelihood of selecting a genotype for migration from a domain population depends upon the degree to which the derived theoretical data associated with that genotype matches the measured data.

4. A method as recited in claim 1, wherein the level of fitness of a genotype is determined by calculating the fitness as a function of the difference between the theoretical data and the measured data.

5. A method as recited in claim 1, wherein the performing step includes reproducing an identical copy of the at least one genotype.

6. A method as recited in claim 1, wherein the performing step includes selecting a gene from the at least one genotype and mutating the gene.

7. A method as recited in claim 1, wherein the performing step includes selecting corresponding genes in a pair of genotypes and exchanging the genes.

8. A method as recited in claim 6, wherein the step of selecting a gene includes randomly selecting the gene.

9. A method as recited in claim 7, wherein the step of selecting corresponding genes includes randomly selecting the genes.

10. A method as recited in claim 1, wherein the step of inspecting includes measuring one wafer at multiple points with data generated from each point being used to define a set of measured data.

11. A method as recited in claim 1, wherein the step of inspecting includes measuring multiple wafers.

12. A multidomain method for evaluating parameters of a semiconductor wafer or wafer set, comprising:

identifying a group of semiconductor wafer parameters to be evaluated;

mapping the semiconductor wafer parameters into at least one genotype, said genotype comprising a collection of genes, each gene corresponding to a selected one of the group of semiconductor wafer parameters to be evaluated;

defining more than one domain as a collection of genotypes, each domain with its own population of genotypes;

deriving a set of theoretical data for each genotype;

inspecting the semiconductor wafer or wafer set using a beam of radiation and generating therefrom sets of measured data;

comparing a set of measured data to a corresponding set of derived theoretical data for each genotype in each domain in order to determine a level of fitness for each genotype;

migrating genotypes among the domains by selecting at least one genotype from a current domain population and adding it to the population of a different domain;

evolving a new population of genotypes for each domain by selecting at least one genotype from the current domain population based on the fitness of the genotype and performing a genetic operation on the at least one genotype to form at least one new genotype, said

genetic operation being selected from one of the following: reproducing an identical copy of the at least one genotype; selecting a gene from the at least one genotype and mutating the gene; or selecting corresponding genes in a pair of genotypes and exchanging the genes, and adding the at least one new genotype to a next population; and

repeating the comparing, migrating, and evolving steps so that for each domain the fittest genotype becomes increasingly more fit.

13. A method as recited in claim 12, wherein the step of selecting at least one genotype for evolution includes selecting at least one genotype in proportion to its fitness.

14. A method as recited in claim 12 wherein the likelihood of selecting a genotype for migration from a domain population depends upon the degree to which the derived theoretical data associated with that genotype matches the measured data.

15. A method as recited in claim 12, wherein the step of selecting a gene includes randomly selecting the gene.

16. A method as recited in claim 12, wherein the step of selecting corresponding genes includes randomly selecting the genes.

17. A multidomain method for evaluating parameters of a semiconductor wafer or wafer set comprising:

identifying a group of semiconductor wafer parameters to be evaluated;

mapping the semiconductor wafer parameters into at least one genotype, said genotype comprising a collection of genes, each gene corresponding to a selected one of the group of semiconductor wafer parameters to be evaluated;

dividing the genes into at least two different gene classes, at least one of said gene classes being subject to a migration operation;

defining more than one domain as a collection of genotypes, each domain with its own population of genotypes;

deriving a set of theoretical data for each genotype;

inspecting the semiconductor wafer or wafer set using a beam of radiation and generating therefrom sets of measured data;

comparing a set of measured data to a corresponding set of derived theoretical data for each genotype in each domain in order to determine a level of fitness for each genotype;

applying a migration operation to at least one genotype from a current domain population, said migration operation including a mechanism for moving genes in at least one of said gene classes to the genotype population of a different domain;

evolving a next population for each domain by selecting at least one genotype from the current population based on the fitness level of the genotype and performing a genetic operation on the at least one genotype, thereby creating at least one new genotype and adding the at least one new genotype to the next population; and

repeating the comparing, migration operation, and evolving steps so that for each domain the fittest genotype becomes increasingly more fit.

18. A method as recited in claim 17 wherein the likelihood of selecting a genotype for a genetic operation from a domain population is proportional to the degree to which the derived theoretical data associated with that genotype matches the measured data.

19. A method as recited in claim 17 wherein the likelihood of selecting a genotype for migration from a domain population depends upon the degree to which the derived theoretical data associated with that genotype matches the measured data.

20. A method as recited in claim 17, wherein the level of fitness of a genotype is determined by calculating the fitness as a function of the difference between the theoretical data and the measured data.

21. A method as recited in claim 17, wherein the performing step includes reproducing an identical copy of the at least one genotype.

22. A method as recited in claim 17, wherein the performing step includes selecting a gene from the at least one genotype and mutating the gene.

23. A method as recited in claim 17, wherein the performing step includes selecting corresponding genes in a pair of genotypes and exchanging the genes.

24. A method as recited in claim 22, wherein the step of selecting a gene includes randomly selecting the gene.

25. A method as recited in claim 23, wherein the step of

selecting corresponding genes includes randomly selecting the genes.

26. A method as recited in claim 17, wherein the permissible range of values for genes in at least one of said gene classes that is subject to a migration operation becomes increasingly narrow as the comparing, migration operation, and evolving steps are repeated.

27. A multidomain method for evaluating parameters of a semiconductor wafer or wafer set, comprising:

identifying a group of semiconductor wafer parameters to be evaluated;

mapping the semiconductor wafer parameters into at least one genotype, said genotype comprising a collection of genes, each gene corresponding to a selected one of the group of semiconductor wafer parameters to be evaluated;

dividing the genes into at least two different gene classes, at least one of said gene classes being subject to a migration operation;

defining more than one domain as a collection of genotypes, each domain with its own population of genotypes;

deriving a set of theoretical data for each genotype;

inspecting the semiconductor wafer or wafer set using a beam of radiation and generating therefrom sets of measured data;

comparing a set of measured data to a corresponding set of derived theoretical data for each genotype in each domain in order to determine a level of fitness for each genotype;

applying a migration operation to at least one genotype from a current domain population, said migration operation including a mechanism for moving genes in at least one of said gene classes to the genotype population of a different domain;

evolving a new population of genotypes for each domain by

selecting at least one genotype from the current domain population based on the fitness of the genotype and performing a genetic operation on the at least one genotype to form at least one new genotype, said genetic operation being selected from one of the following: reproducing an identical copy of the at least one genotype; selecting a gene from the at least one genotype and mutating the gene; or selecting corresponding genes in a pair of genotypes and exchanging the genes, and adding the at least one new genotype to a next population; and

repeating the comparing, migration operation, and evolving steps so that for each domain the fittest genotype becomes increasingly more fit.

28. A method as recited in claim 27, wherein the step of selecting at least one genotype for evolution includes selecting at least one genotype in proportion to its fitness.

29. A method as recited in claim 27 wherein the likelihood of selecting a genotype for migration from a domain population depends upon the degree to which the derived theoretical data associated with that genotype matches the measured data.

30. A method as recited in claim 27, wherein the step of selecting a gene includes randomly selecting the gene.

31. A method as recited in claim 27, wherein the step of selecting corresponding genes includes randomly selecting the genes.

32. A method as recited in claim 27, wherein the permissible

range of values for genes in at least one of said gene classes that is subject to a migration operation becomes increasingly narrow as the comparing, migration operation, and evolving steps are repeated.

33. A method as recited in claim 1 or claim 12 or claim 17 or claim 27 wherein the step of deriving a set of theoretical data for each genotype includes the use of a nonlinear least squares optimization algorithm for selected genotypes.

34. A multidomain process for evaluating parameters of a semiconductor wafer or wafer set comprising:

identifying a group of semiconductor wafer parameters to be evaluated;

inspecting the semiconductor wafer or wafer set using a beam of radiation and generating therefrom sets of measured data, each set of measured data corresponding to a different measurement;

defining more than one search domain, each search domain corresponding to a set of measured data;

applying an iterative search method to each search domain in order to generate a group of optimized parameter values for each search domain, said iterative search method including the steps of:

generating a set of theoretical parameter values associated with each search domain;

deriving a set of theoretical data for each set of theoretical parameter values;

comparing the sets of theoretical data associated with the set of parameter values associated with each search domain to the set of measured data corresponding to each search domain;

generating a new set of theoretical parameter values of each search domain based on the comparing step in a manner so as to identify increasingly more optimal theoretical parameter

values for each search domain; and

wherein said iterative search method further includes the step of migrating a set of theoretical parameter values from one search domain to another search domain.

35. A method as recited in claim 34, wherein the step of inspecting includes measuring one wafer at multiple points.

36. A method as recited in claim 34, wherein the step of inspecting includes measuring multiple wafers.

37. A method as recited in claim 34 wherein said iterative search method is a genetic algorithm.